

RAW SEQUENCE LISTING

DATE: 10/01/2001

PATENT APPLICATION: US/09/617,923

TIME: 12:12:46

Input Set : N:\Crf3\RULE60\09617923.txt

Output Set: N:\CRF3\10012001\I617923.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Glimcher, Laurie H.

7 Hodge, Martin R.

9 (ii) TITLE OF INVENTION: NF-AT-INTERACTING PROTEIN NIP45 AND METHODS

10 OF USE THEREFOR

12 (iii) NUMBER OF SEQUENCES: 2

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: LAHIVE & COCKFIELD

16 (B) STREET: 60 State Street, suite 510

17 (C) CITY: Boston

18 (D) STATE: Massachusetts

19 (E) COUNTRY: USA

20 (F) ZIP: 02109-1875

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/617,923

C--> 30 (B) FILING DATE: 17-Jul-2000

31 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 08/755,584

35 (B) FILING DATE: 25-NOV-1996

37 (viii) ATTORNEY/AGENT INFORMATION:

38 (A) NAME: Giulio A. DeConti, Jr.

39 (B) REGISTRATION NUMBER: 31,503

40 (C) REFERENCE/DOCKET NUMBER: HUI-026

42 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: (617)227-7400

44 (B) TELEFAX: (617)227-5941

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 1946 base pairs

51 (B) TYPE: nucleic acid

52 (C) STRANDEDNESS: single

53 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

57 (ix) FEATURE:

58 (A) NAME/KEY: CDS

59 (B) LOCATION: 13..1248

62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

64 ACAGTGTGGG AG ATG GCG GAA CCA CTG AGG GGA CGT GGT CCG AGG TCC 48

65 Met Ala Glu Pro Leu Arg Gly Arg Gly Pro Arg Ser

66

1

5

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68	CGC	GGT	GGC	CGA	GGC	GCT	CGG	AGA	GCC	CGA	GGC	GCC	CGT	GGC	CGG	TGT	96
69	Arg	Gly	Gly	Arg	Gly	Ala	Arg	Arg	Ala	Arg	Gly	Ala	Arg	Gly	Arg	Cys	
70		15					20					25					
72	CCT	CGC	GCC	CGG	CAG	TCT	CCG	GCT	AGG	CTC	ATT	CCA	GAC	ACC	GTG	CTT	144
73	Pro	Arg	Ala	Arg	Gln	Ser	Pro	Ala	Arg	Leu	Ile	Pro	Asp	Thr	Val	Leu	
74		30					35					40					
76	GTG	GAC	TTG	GTC	AGT	GAC	AGC	GAC	GAA	GAG	GTC	TTG	GAA	GTC	GCA	GAC	192
77	Val	Asp	Leu	Val	Ser	Asp	Ser	Asp	Glu	Glu	Val	Leu	Glu	Val	Ala	Asp	
78	45				50					55				60			
80	CCA	GTA	GAG	GTG	CCG	GTC	GCC	CGC	CTC	CCC	GCG	CCG	GCT	AAA	CCT	GAG	240
81	Pro	Val	Glu	Val	Pro	Val	Ala	Arg	Leu	Pro	Ala	Pro	Ala	Lys	Pro	Glu	
82					65					70				75			
84	CAG	GAC	AGC	GAC	AGT	GAC	AGT	GAA	GGG	GCG	GCC	GAG	GGG	CCT	GCG	GGA	288
85	Gln	Asp	Ser	Asp	Ser	Asp	Ser	Glu	Gly	Ala	Ala	Glu	Gly	Pro	Ala	Gly	
86			80					85				90					
88	GCC	CCG	CGT	ACA	TTG	GTG	CGA	CGG	CGG	CGG	CGG	CTG	CTG	GAT	CCC		336
89	Ala	Pro	Arg	Thr	Leu	Val	Arg	Arg	Arg	Arg	Arg	Leu	Leu	Asp	Pro		
90			95				100					105					
92	GGA	GAG	GCG	CCG	GTG	GTC	CCA	GTG	TAC	TCC	GGG	AAG	GTA	CAG	AGC	AGC	384
93	Gly	Glu	Ala	Pro	Val	Val	Pro	Val	Tyr	Ser	Gly	Lys	Val	Gln	Ser	Ser	
94		110					115					120					
96	CTC	AAC	CTC	ATT	CCA	GAT	AAT	TCA	TCC	CTC	TTG	AAA	CTG	TGC	CCT	TCA	432
97	Leu	Asn	Leu	Ile	Pro	Asp	Asn	Ser	Ser	Leu	Leu	Lys	Leu	Cys	Pro	Ser	
98	125				130					135				140			
100	GAG	CCT	GAA	GAT	GAG	GCA	GAT	CTG	ACA	AAT	TCT	GGC	AGT	TCT	CCC	TCT	480
101	Glu	Pro	Glu	Asp	Glu	Ala	Asp	Leu	Thr	Asn	Ser	Gly	Ser	Ser	Pro	Ser	
102					145					150				155			
104	GAG	GAT	GAT	GCC	CTG	CCT	TCA	GGT	TCT	CCC	TGG	AGA	AAG	AAG	CTC	AGA	528
105	Glu	Asp	Asp	Ala	Leu	Pro	Ser	Gly	Ser	Pro	Trp	Arg	Lys	Lys	Leu	Arg	
106			160					165				170					
108	AAG	AAG	TGT	GAG	AAA	GAA	GAA	AAG	AAA	ATG	GAA	GAG	TTT	CCG	GAC	CAG	576
109	Lys	Lys	Cys	Glu	Lys	Glu	Glu	Lys	Lys	Met	Glu	Glu	Phe	Pro	Asp	Gln	
110			175					180				185					
112	GAC	ATC	TCT	CCT	TTG	CCC	CAA	CCT	TCG	TCA	AGG	AAC	AAA	AGC	AGA	AAG	624
113	Asp	Ile	Ser	Pro	Leu	Pro	Gln	Pro	Ser	Ser	Arg	Asn	Lys	Ser	Arg	Lys	
114		190					195					200					
116	CAT	ACG	GAG	GCG	CTC	CAG	AAG	CTA	AGG	GAA	GTG	AAC	AAG	CGT	CTC	CAA	672
117	His	Thr	Glu	Ala	Leu	Gln	Lys	Leu	Arg	Glu	Val	Asn	Lys	Arg	Leu	Gln	
118	205				210					215				220			
120	GAT	CTC	CGC	TCC	TGC	CTG	AGC	CCC	AAG	CAG	CAC	CAG	AGT	CCA	GCC	CTT	720
121	Asp	Leu	Arg	Ser	Cys	Leu	Ser	Pro	Lys	Gln	His	Gln	Ser	Pro	Ala	Leu	
122					225					230				235			
124	CAG	AGC	ACA	GAT	GAT	GAG	GTG	GTC	CTA	GTG	GAA	GGG	CCT	GTC	TTG	CCA	768
125	Gln	Ser	Thr	Asp	Asp	Glu	Val	Val	Leu	Val	Glu	Gly	Pro	Val	Leu	Pro	
126			240					245				250					
128	CAG	AGC	TCT	CGA	CTC	TTT	ACA	CTC	AAG	ATC	CGG	TGC	CGG	GCT	GAC	CTA	816
129	Gln	Ser	Ser	Arg	Leu	Phe	Thr	Leu	Lys	Ile	Arg	Cys	Arg	Ala	Asp	Leu	
130			255					260				265					
132	GTG	AGA	CTG	CCT	GTC	AGG	ATG	TCG	GAG	CCC	CTT	CAG	AAT	GTG	GTG	GAT	864

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```

133 Val Arg Leu Pro Val Arg Met Ser Glu Pro Leu Gln Asn Val Val Asp
134      270                      275                      280
136 CAC ATG GCC AAT CAT CTT GGG GTG TCT CCA AAC AGG ATT CTT TTG CTT      912
137 His Met Ala Asn His Leu Gly Val Ser Pro Asn Arg Ile Leu Leu Leu
138 285                      290                      295                      300
140 TTT GGA GAG AGT GAA CTG TCT CCT ACT GCC ACC CCT AGT ACC CTA AAG      960
141 Phe Gly Glu Ser Glu Leu Ser Pro Thr Ala Thr Pro Ser Thr Leu Lys
142                      305                      310                      315
144 CTT GGA GTG GCT GAC ATC ATT GAT TGT GTG GTG CTA GCA AGC TCT TCA      1008
145 Leu Gly Val Ala Asp Ile Ile Asp Cys Val Val Leu Ala Ser Ser Ser
146                      320                      325                      330
148 GAG GCC ACA GAG ACA TCC CAG GAG CTC CGG CTC CGG GTG CAG GGG AAG      1056
149 Glu Ala Thr Glu Thr Ser Gln Glu Leu Arg Leu Arg Val Gln Gly Lys
150                      335                      340                      345
152 GAG AAA CAC CAG ATG TTG GAG ATC TCA CTG TCT CCT GAT TCT CCT CTT      1104
153 Glu Lys His Gln Met Leu Glu Ile Ser Leu Ser Pro Asp Ser Pro Leu
154                      350                      355                      360
156 AAG GTT CTC ATG TCA CAC TAT GAG GAA GCC ATG GGA CTC TCT GGA CAC      1152
157 Lys Val Leu Met Ser His Tyr Glu Glu Ala Met Gly Leu Ser Gly His
158 365                      370                      375                      380
160 AAG CTC TCC TTC TTC TTT GAT GGG ACA AAG CTT TCA GGC AAG GAG CTG      1200
161 Lys Leu Ser Phe Phe Phe Asp Gly Thr Lys Leu Ser Gly Lys Glu Leu
162                      385                      390                      395
164 CCA GCT GAT CTG GGC CTG GAA TCC GGA GAT CTC ATC GAA GTC TGG GGC      1248
165 Pro Ala Asp Leu Gly Leu Glu Ser Gly Asp Leu Ile Glu Val Trp Gly
166                      400                      405                      410
168 TGAAGCTCTC ACCCTGTTTCG GACGCAAAGC CAAGACATGG AGACAATAGC TCCCAATTTT      1308
170 ATTATTGTGA TTTTTCGCCC CATAAGGGCT AACAGAAACT GAATTAGAAC TTGTTTACTT      1368
172 ATTTATTTCT GGTGCTGGGG ATTGAACCCC AGACTATGCA CATGCTAAGG ATGTATGAAG      1428
174 TGGAGGCAAA ACCAAGGCAT TACCTTTAGC CAGCCTCTAG TAGACTGTAG TGTC AAGCAA      1488
176 GTGGCTACTT GGTAGTTGTG TGGCTCTGTG TATGTTTGTG CTGTATTTGG CAGCCCCTGG      1548
178 GGCACATAGA AGGGACCTTG GCTTCCCTAC CATTTCACGT TCGCTGGTGC CCTTTCCTTC      1608
180 ATCAGATGAC TTCTGTGAAG CTGCCTATGT TGAGTGTGTT GAACTAAATG AGCTCTGCTT      1668
182 TGGGTGTCCA GGCCTGGGGT TTGTGCCGCA GTTGGAGCCA GCAGTGACTT CACTTGACT      1728
184 TGGGACTGAG AATGCATTTT CTGGTGGAGA CACTCGGGTG CAGAAATATA ACAGAAGGTG      1788
186 ACATACATGC TGAAGCTGAG GACTAGGTCG AAAGTTAACG ACGTTGCATT TTCAGCCTTG      1848
188 GGTATCCTCT CTGCCTGCCA GGACTCTAGC CAGTGTCTGG TACACACTTC TTGGCATGGA      1908
190 CACCTAGGTC GACGCGGGCG CGATTGCGCC GACTCGAG      1946
193 (2) INFORMATION FOR SEQ ID NO: 2:
195     (i) SEQUENCE CHARACTERISTICS:
196         (A) LENGTH: 412 amino acids
197         (B) TYPE: amino acid
198         (D) TOPOLOGY: linear
200     (ii) MOLECULE TYPE: protein
202     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
204 Met Ala Glu Pro Leu Arg Gly Arg Gly Pro Arg Ser Arg Gly Gly Arg
205  1      5      10      15
207 Gly Ala Arg Arg Ala Arg Gly Ala Arg Gly Arg Cys Pro Arg Ala Arg
208      20      25      30

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```

210 Gln Ser Pro Ala Arg Leu Ile Pro Asp Thr Val Leu Val Asp Leu Val
211      35      40      45
213 Ser Asp Ser Asp Glu Glu Val Leu Glu Val Ala Asp Pro Val Glu Val
214      50      55      60
216 Pro Val Ala Arg Leu Pro Ala Pro Ala Lys Pro Glu Gln Asp Ser Asp
217      65      70      75      80
219 Ser Asp Ser Glu Gly Ala Ala Glu Gly Pro Ala Gly Ala Pro Arg Thr
220      85      90      95
222 Leu Val Arg Arg Arg Arg Arg Arg Leu Leu Asp Pro Gly Glu Ala Pro
223      100     105     110
225 Val Val Pro Val Tyr Ser Gly Lys Val Gln Ser Ser Leu Asn Leu Ile
226      115     120     125
228 Pro Asp Asn Ser Ser Leu Leu Lys Leu Cys Pro Ser Glu Pro Glu Asp
229      130     135     140
231 Glu Ala Asp Leu Thr Asn Ser Gly Ser Ser Pro Ser Glu Asp Asp Ala
232 145      150      155      160
234 Leu Pro Ser Gly Ser Pro Trp Arg Lys Lys Leu Arg Lys Lys Cys Glu
235      165     170     175
237 Lys Glu Glu Lys Lys Met Glu Glu Phe Pro Asp Gln Asp Ile Ser Pro
238      180     185     190
240 Leu Pro Gln Pro Ser Ser Arg Asn Lys Ser Arg Lys His Thr Glu Ala
241      195     200     205
243 Leu Gln Lys Leu Arg Glu Val Asn Lys Arg Leu Gln Asp Leu Arg Ser
244      210     215     220
246 Cys Leu Ser Pro Lys Gln His Gln Ser Pro Ala Leu Gln Ser Thr Asp
247 225      230      235      240
249 Asp Glu Val Val Leu Val Glu Gly Pro Val Leu Pro Gln Ser Ser Arg
250      245     250     255
252 Leu Phe Thr Leu Lys Ile Arg Cys Arg Ala Asp Leu Val Arg Leu Pro
253      260     265     270
255 Val Arg Met Ser Glu Pro Leu Gln Asn Val Val Asp His Met Ala Asn
256      275     280     285
258 His Leu Gly Val Ser Pro Asn Arg Ile Leu Leu Leu Phe Gly Glu Ser
259      290     295     300
261 Glu Leu Ser Pro Thr Ala Thr Pro Ser Thr Leu Lys Leu Gly Val Ala
262 305      310      315      320
264 Asp Ile Ile Asp Cys Val Val Leu Ala Ser Ser Ser Glu Ala Thr Glu
265      325      330      335
267 Thr Ser Gln Glu Leu Arg Leu Arg Val Gln Gly Lys Glu Lys His Gln
268      340      345      350
270 Met Leu Glu Ile Ser Leu Ser Pro Asp Ser Pro Leu Lys Val Leu Met
271      355      360      365
273 Ser His Tyr Glu Glu Ala Met Gly Leu Ser Gly His Lys Leu Ser Phe
274      370      375      380
276 Phe Phe Asp Gly Thr Lys Leu Ser Gly Lys Glu Leu Pro Ala Asp Leu
277 385      390      395      400
279 Gly Leu Glu Ser Gly Asp Leu Ile Glu Val Trp Gly
280      405      410

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VERIFICATION SUMMARY

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Input Set : N:\CrF3\RULE60\09617923.txt

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]